

SEQUENCE LISTING

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Freidrich, Glenn A.
Sands, Arthur T.

<120> A NOVEL HUMAN cDNA CLONE AND PROTEINS
ENCODED THEREBY

<130> 8535-0036-888

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<170> FastSEQ for Windows Version 3.0

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<211> 1116

<212> DNA

<213> Homo sapien

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<221> CDS

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tgg gaa act cgt gtc aag aag cac aaa gct tgg cag aag aag gag gtg	96
Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val	
20 25 30	
gaa agg ctt gag aag agc gcc ttg gag aag ata aag gag gag tgg aac	144
Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn	
35 40 45	
ttt gtg gcc gaa tgc agg agg aag ggc atc ccc cag gct gta tac tgc	192
Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys	
50 55 60	
aag aat ggc ttc ata gac acc agc gtg cgg ctt ctg gac aag att gaa	240
Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu	
65 70 75 80	
agg aac act ctc aca agg cag agt tca ctt ccc aag gac aga ggc aaa	288
Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys	
85 90 95	
cgg agc agt gcg ttt gtg ttt gaa ctt tct ggg gag cac tgg acg gag	336
Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu	
100 105 110	

ctc cca gat tca ttg aag gag cag aca cac ctg aga gaa tgg tac ata	384
Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile	
115 120 125	
agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432
Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln	
130 135 140	
gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca	480
Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro	
145 150 155 160	
gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc	528
Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe	
165 170 175	
aac tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta	576
Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu	
180 185 190	
gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt	624
Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe	
195 200 205	
gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac	672
Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn	
210 215 220	
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Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln	
225 230 235 240	
tgg ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata	768
Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile	
245 250 255	
gac agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg	816
Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu	
260 265 270	
acc tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta	864
Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu	
275 280 285	
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Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp	
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tca tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat	960
Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp	
305 310 315 320	
aat gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat	1008
Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp	
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135

140

gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca 480
 Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
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tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat 528
 Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
 165 170 175

gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc 576
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 180 185 190

caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa 624
 Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
 195 200 205

gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt 672
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 Gln Leu
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<212> PRT

<213> Homo sapien

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 Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
 35 40 45
 Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
 50 55 60
 Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
 65 70 75 80
 Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
 85 90 95
 Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
 100 105 110
 Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
 115 120 125
 Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
 130 135 140
 Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
 145 150 155 160
 Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
 165 170 175
 Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg

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		195					200					205		
Glu	Arg	Glu	Ser	Val	Pro	Ser	Tyr	Thr	Thr	Lys	Val	Ser	Phe	Ser
	210					215					220			
Gln	Leu													
225														